SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: BASF Aktiengesellschaft
(B) STREET: Carl-Bosch-Strasse 38
(C) CITY: Ludwigshafen
(E) COUNTRY: Federal Republic of Germany
(F) POSTAL CODE: D-67056
(G) TELEPHONE: 0621/6048526
(H) TELEFAX: 0621/6043123
(I) TELEX: 1762175170

(ii) TITLE OF APPLICATION: Method for diagnosing disorders by analysis of genes

(iii) NUMBER OF SEQUENCES: 2

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPA)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1517 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA for mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURES:

(A) NAME/KEY: CDS
(B) LOCATION: 1..1024

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```
ATG GGG GAG ATG GAG CAA CTG CGT CAG GAA GCG GAG CAG CTC AAG AAG    48
Met Gly Glu Met Glu Gln Leu Arg Gln Glu Ala Glu Gln Leu Lys Lys
 1               5                  10                  15
CAG ATT GCA GAT GCC AGG AAA GCC TGT GCT GAC GTT ACT CTG GCA GAG    96
Gln Ile Ala Asp Ala Arg Lys Ala Cys Ala Asp Val Thr Leu Ala Glu
            20                  25                  30
CTG GTG TCT GGC CTA GAG GTG GTG GGA CGA GTC CAG ATG CGG ACG CGG   144
Leu Val Ser Gly Leu Glu Val Val Gly Arg Val Gln Met Arg Thr Arg
        35                  40                  45
CGG ACG TTA AGG GGA CAC CTG GCC AAG ATT TAC GCC ATG CAC TGG GCC   192
Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr Ala Met His Trp Ala
    50                  55                  60
ACT GAT TCT AAG CTG CTG GTA AGT GCC TCG CAA GAT GGG AAG CTG ATC   240
Thr Asp Ser Lys Leu Leu Val Ser Ala Ser Gln Asp Gly Lys Leu Ile
65                  70                  75                  80
GTG TGG GAC AGC TAC ACC ACC AAC AAG GTG CAC GCC ATC CCA CTG CGC   288
Val Trp Asp Ser Tyr Thr Thr Asn Lys Val His Ala Ile Pro Leu Arg
                85                  90                  95
TCC TCC TGG GTC ATG ACC TGT GCC TAT GCC CCA TCA GGG AAC TTT GTG   336
Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro Ser Gly Asn Phe Val
```

```
                100                 105                 110
GCA TGT GGG GGG CTG GAC AAC ATG TGT TCC ATC TAC AAC CTC AAA TCC    384
Ala Cys Gly Gly Leu Asp Asn Met Cys Ser Ile Tyr Asn Leu Lys Ser
        115                 120                 125
CGT GAG GGC AAT GTC AAG GTC AGC CGG GAG CTT TCT GCT CAC ACA GGT    432
Arg Glu Gly Asn Val Lys Val Ser Arg Glu Leu Ser Ala His Thr Gly
    130                 135                 140
TAT CTC TCC TGC TGC CGC TTC CTG GAT GAC AAC AAT ATT GTG ACC AGC    480
Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn Asn Ile Val Thr Ser
145                 150                 155                 160
TCG GGG GAC ACC ACG TGT GCC TTG TGG GAC ATT GAG ACT GGG CAG CAG    528
Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp Ile Glu Thr Gly Gln Gln
                165                 170                 175
AAG ACT GTA TTT GTG GGA CAC ACG GGT GAC TGC ATG AGC CTG GCT GTG    576
Lys Thr Val Phe Val Gly His Thr Gly Asp Cys Met Ser Leu Ala Val
            180                 185                 190
TCT CCT GAC TTC AAT CTC TTC ATT TCG GGG GCC TGT GAT GCC AGT GCC    624
Ser Pro Asp Phe Asn Leu Phe Ile Ser Gly Ala Cys Asp Ala Ser Ala
        195                 200                 205
AAG CTC TGG GAT GTG CGA GAG GGG ACC TGC CGT CAG ACT TTC ACT GGC    672
Lys Leu Trp Asp Val Arg Glu Gly Thr Cys Arg Gln Thr Phe Thr Gly
    210                 215                 220
CAC GAG TCG GAC ATC AAC GCC ATC TGT TTC TTC CCC AAT GGA GAG GCC    720
His Glu Ser Asp Ile Asn Ala Ile Cys Phe Phe Pro Asn Gly Glu Ala
225                 230                 235                 240
ATC TGC ACG GGC TCG GAT GAC GCT TCC TGC CGC TTG TTT GAC CTG CGG    768
Ile Cys Thr Gly Ser Asp Asp Ala Ser Cys Arg Leu Phe Asp Leu Arg
                245                 250                 255
GCA GAC CAG GAG CTG ATC TGC TTC TCC CAC GAG AGC ATC ATC TGC GGC    816
Ala Asp Gln Glu Leu Ile Cys Phe Ser His Glu Ser Ile Ile Cys Gly
            260                 265                 270
ATC ACG TCT GTG GCC TTC TCC CTC AGT GGC CGC CTA CTA TTC GCT GGC    864
Ile Thr Ser Val Ala Phe Ser Leu Ser Gly Arg Leu Leu Phe Ala Gly
        275                 280                 285
TAC GAC GAC TTC AAC TGC AAT GTC TGG GAC TCC ATG AAG TCT GAG CGT    912
Tyr Asp Asp Phe Asn Cys Asn Val Trp Asp Ser Met Lys Ser Glu Arg
    290                 295                 300
GTG GGC ATC CTC TCT GGC CAC GAT AAC AGG GTG AGC TGC CTG GGA GTC    960
Val Gly Ile Leu Ser Gly His Asp Asn Arg Val Ser Cys Leu Gly Val
305                 310                 315                 320
ACA GCT GAC GGG ATG GCT GTG GCC ACA GGT TCC TGG GAC AGC TTC CTC   1008
Thr Ala Asp Gly Met Ala Val Ala Thr Gly Ser Trp Asp Ser Phe Leu
                325                 330                 335
AAA ATC TGG AAC TGA G GAGGCTGGAG AAAGGGAAGT GGAAGGCAGT GAAGACACTC 1064
Lys Ile Trp Asn  *
            340
AGCAGCCCCC TGCCCGACCC CATCTCATTC AGGTGTTCTC TTCTATATTC CGGGTGCCAT 1124
TCCCACTAAG CTTTCTCCTT TGAGGGCAGT GGGGAGCATG GGACTGTGCC TTTGGGAGGC 1184
AGCATCAGGG ACACAGGGGC AAAGAACTGC CCCATCTCCT CCCATGGCCT TCCCTCCCCA 1244
CAGTCCTCAC AGCCTCTCCC TTAATGAGCA AGGACAACCT GCCCCTCCCC AGCCCTTTGC 1304
AGGCCCAGCA GACTTGAGTC TGAGGCCCCA GGCCCTAGGA TTCCTCCCCC AGAGCCACTA 1364
CCTTTGTCCA GGCCTGGGTG GTATAGGGCG TTTGGCCCTG TGACTATGGC TCTGGCACCA 1424
CTAGGGTCCT GGCCCTCTTC TTATTCATGC TTTCTCCTTT TTCTACCTTT TTTTCTCTCC 1484
TAAGACACCT GCAATAAAGT GTAGCACCCT GGT                              1517
```

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 341 amino acids

(B) TYPE: Amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
Met Gly Glu Met Glu Gln Leu Arg Gln Glu Ala Glu Gln Leu Lys Lys
 1               5                  10                  15
Gln Ile Ala Asp Ala Arg Lys Ala Cys Ala Asp Val Thr Leu Ala Glu
            20                  25                  30
Leu Val Ser Gly Leu Glu Val Val Gly Arg Val Gln Met Arg Thr Arg
        35                  40                  45
Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr Ala Met His Trp Ala
    50                  55                  60
Thr Asp Ser Lys Leu Leu Val Ser Ala Ser Gln Asp Gly Lys Leu Ile
65                  70                  75                  80
Val Trp Asp Ser Tyr Thr Thr Asn Lys Val His Ala Ile Pro Leu Arg
                85                  90                  95
Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro Ser Gly Asn Phe Val
            100                 105                 110
Ala Cys Gly Gly Leu Asp Asn Met Cys Ser Ile Tyr Asn Leu Lys Ser
        115                 120                 125
Arg Glu Gly Asn Val Lys Val Ser Arg Glu Leu Ser Ala His Thr Gly
    130                 135                 140
Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn Asn Ile Val Thr Ser
145                 150                 155                 160
Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp Ile Glu Thr Gly Gln Gln
                165                 170                 175
Lys Thr Val Phe Val Gly His Thr Gly Asp Cys Met Ser Leu Ala Val
            180                 185                 190
Ser Pro Asp Phe Asn Leu Phe Ile Ser Gly Ala Cys Asp Ala Ser Ala
        195                 200                 205
Lys Leu Trp Asp Val Arg Glu Gly Thr Cys Arg Gln Thr Phe Thr Gly
    210                 215                 220
His Glu Ser Asp Ile Asn Ala Ile Cys Phe Phe Pro Asn Gly Glu Ala
225                 230                 235                 240
Ile Cys Thr Gly Ser Asp Asp Ala Ser Cys Arg Leu Phe Asp Leu Arg
                245                 250                 255
Ala Asp Gln Glu Leu Ile Cys Phe Ser His Glu Ser Ile Ile Cys Gly
            260                 265                 270
Ile Thr Ser Val Ala Phe Ser Leu Ser Gly Arg Leu Leu Phe Ala Gly
        275                 280                 285
Tyr Asp Asp Phe Asn Cys Asn Val Trp Asp Ser Met Lys Ser Glu Arg
    290                 295                 300
Val Gly Ile Leu Ser Gly His Asp Asn Arg Val Ser Cys Leu Gly Val
305                 310                 315                 320
Thr Ala Asp Gly Met Ala Val Ala Thr Gly Ser Trp Asp Ser Phe Leu
                325                 330                 335
Lys Ile Trp Asn  *
            340
```

We claim:

1. The use of a genetic modification in the gene for human G protein β3 subunit for the diagnosis of diseases.

2. The use of a genetic modification in the gene for human G protein β3 subunit for establishing the risk of developing a disorder associated with G protein dysregulation.

3. The use as claimed in claim 2, wherein the genetic modification is in the codon for amino acid 275 in SEQ ID NO:1.

4. The use as claimed in claim 3, wherein there is substitution of cytosine by thymine in position 825 in SEQ ID NO:1.

5. The use as claimed in claim 2, wherein the disorder is a cardiovascular disease, a metabolic disturbance or an immunological disease.

6. The use as claimed in claim 2, wherein the disorder is hypertension.

7. A method for establishing a relative risk of developing disorders associated with G protein dysregulation for a subject, which comprises comparing the gene sequence for human G protein β3 subunit of the subject with the gene sequence SEQ ID NO:1, and, in the event that a thymine (T) is present at position 825, assigning the subject an increased risk of disease.

8. A method as claimed in claim 7, wherein the comparison of genes is carried out by sequencing.

9. A method as claimed in claim 8, wherein a gene section which includes position 825 is amplified before the sequencing.

10. A method as claimed in claim 7, wherein the comparison of genes is carried out by hybridization.

11. A method as claimed in claim 7, wherein the comparison of genes is carried out by cleavage using restriction enzymes.

12. A method as claimed in claim 11, wherein the restriction enzyme Dsa I is used.

The use of a genetic modification in the gene for human G protein β3 subunit for the diagnosis of diseases

Abstract

The present invention relates to the use of a genetic modification in the gene for human G protein β3 subunit for the diagnosis of diseases.